

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217  
gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761  
Length = 411

Score = 783 bits (2023), Expect = 0.0  
Identities = 410/411 (99%), Positives = 411/411 (100%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60  
MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII  
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120  
GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT  
Sbjct: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120

Query: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
Sbjct: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD 240  
LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD  
Sbjct: 181 LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300  
AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS  
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ 360  
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ  
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTL SVNHLTNERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411  
ELTPCRRTL SVNHLT+ERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK  
Sbjct: 361 ELTPCRRTL SVNHLT SERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411

>gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217  
Length = 411

Score = 764 bits (1974), Expect = 0.0  
Identities = 394/411 (95%), Positives = 406/411 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60  
MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKT VSTIFLVVLYLII  
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKT VSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120  
GA VFKALEQP EISQRTTIVI QKQTFI+QH+CVNSTELDELIQQIVAAINAGI IPLGN+  
Sbjct: 61 GAAVFKALEQPQEISQRTTIVI QKQTFIAQHACVNSTELDELIQQIVAAINAGI IPLGNS 120

Query: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
  
 Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIFKHIEGWSALD 240  
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD  
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
  
 Query: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS  
 Sbjct: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
  
 Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360  
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ  
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
  
 Query: 361 ELTPCRRTLSVNHLTNERDVLPLLLKTESIYLNGLTPHCAGEEIAVIENIK 411  
 ELTPC RTLSVNHLT+ER+VLPLLLK ESIYLNGLTPHCAGE+IAVIEN+K  
 Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPLLLKAESIYLNGLTPHCAGEDIAVIENMK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]  
 Length = 370

Score = 684 bits (1766), Expect = 0.0  
 Identities = 356/368 (96%), Positives = 364/368 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDITINVMKWKTVSTIFLVVLYLII 60  
 MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVLYLII  
 Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
  
 Query: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120  
 GA VFKALEQP EISQRTTIVIQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT+  
 Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120  
  
 Query: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
 SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
  
 Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIFKHIEGWSALD 240  
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD  
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
  
 Query: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS  
 Sbjct: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
  
 Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360  
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ  
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
  
 Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

&gt;gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855

Length = 370

Score = 681 bits (1758), Expect = 0.0

Identities = 355/368 (96%), Positives = 363/368 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
 MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVLYLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120  
 GA VFKALEQP EISQRTTIVIQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT+

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQISHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
 SNQ+SHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL GFLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD

Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360  
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ

Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368  
 ELTPC RT

Sbjct: 361 ELTPCMRT 368

INSTANT  
SEQ ID NO: 4

gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217  
Length = 411

Score = 784 bits (2025), Expect = 0.0  
Identities = 410/411 (99%), Positives = 410/411 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII  
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120  
GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS  
Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
LGTIFGKGIKVEDTFIKWNVSTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD  
Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS  
Sbjct: 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ  
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411  
ELTPC RTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK  
Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217  
gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761  
Length = 411

Score = 768 bits (1984), Expect = 0.0  
Identities = 396/411 (96%), Positives = 407/411 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVLYLII  
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD+TTINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120  
GA VFKALEQP EISQRTTIVIQQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT  
Sbjct: 61 GATVFKALEQPHEISQRTTIVIQQTFISQHSVCVNSTELDELIQQIVAAINAGIIPLGNT 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
 Sbjct: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD  
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300  
 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS  
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ  
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYNGLTPHCAGEDIAVIENMK 411  
 ELTPCRRTLSVNHLTSE+VLPPLLK ESIYNGLTPHCAGE+IAVIEN+K  
 Sbjct: 361 ELTPCRRTLSVNHLTSE+VLPPLLKTESIYNGLTPHCAGEEIAVIENIK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]  
 Length = 370

Score = 696 bits (1797), Expect = 0.0  
 Identities = 367/368 (99%), Positives = 367/368 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII  
 Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120  
 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS  
 Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ  
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD  
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300  
 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS  
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ  
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368

## ELTPC RT

Sbjct: 361 ELTPCMRT 368

&gt;gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855

Length = 370

Score = 693 bits (1789), Expect = 0.0

Identities = 366/368 (99%), Positives = 366/368 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120  
GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180  
SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL G FLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLG FLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD

Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360  
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

DIFFERENT FROM SEQ ID NO:4 at residue 366:

L5 ANSWER 2 OF 3 DGENE COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: AAY28497 Protein DGENE

TITLE: New two pore potassium channel used for, e.g.

treatment of

cancer, pulmonary, cardiovascular and inflammatory

diseases

INVENTOR: Chapman C G; Meadows H J

PATENT ASSIGNEE: (SMIK) SMITHKLINE BEECHAM PLC.

PATENT INFO: WO 9937762 A1 19990729

44p

APPLICATION INFO: WO 1998-EP7805 19981202

PRIORITY INFO: GB 1998-22135 19981009

EP 1998-300570 19980127

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1999-469126 [39]

CROSS REFERENCES: N-PSDB: AAZ00040

DESCRIPTION: Mouse h-TREK1 polypeptide.

AN AAY28497 Protein DGENE

AA 37 A; 14 R; 14 N; 14 D; 0 B; 5 C; 14 Q; 23 E; 0 Z; 28 G; 7 H;  
42 I;

39 L; 23 K; 5 M; 25 F; 14 P; 29 S; 27 T; 8 W; 9 Y; 34 V; 0

Others

SQL 411

SEQ

1 maapdlldpk saaqnskpri sfsskptvla srvesdsain vmkwktvsti

51 flvvvlylii gaavfkaleq pqueisqrtdi viqkqtfiaq hacvnsteld

=====

101 eliqqivaai nagiipngs snqvshwdlg ssffagatvi ttigfgnisp

151 rteggkifci iyallgipfl gfillagvgdq lgtifgkgia kvedtfikwn

201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiylfvitlt

251 tigfgdyvag gsdieyldfy kpvvfwilv glayfaavls migdwlrvls

301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl

351 saelagnhnq eltpcmrtls vnhltserev lppllkaesi ylngltphca

401 gediavienm k

HITS AT: 65-76

1 maapdlldpk saaqnskpri sfsskptvla srvesdsain vmkwktvsti

51 flvvvlylii gaavfkaleq pqueisqrtdi viqkqtfiaq hacvnsteld

101 eliqqivaai nagiipngs snqvshwdlg ssffagatvi ttigfgnisp

151 rteggkifci iyallgipfl gfillagvgdq lgtifgkgia kvedtfikwn

201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiylfvitlt

251 tigfgdyvag gsdieyldfy kpvvfwilv glayfaavls migdwlrvls

301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl

351 saelagnhnq eltpcmrtls vnhltserev lppllkaesi ylngltphca

401 gediavienm k

L11 ANSWER 23 OF 33 PCTFULL COPYRIGHT 2003 Univentio on STN  
ACCESSION NUMBER: 2001046258 PCTFULL ED 20020827  
TITLE (ENGLISH): TRANSPORTERS AND ION CHANNELS  
TITLE (FRENCH): TRANSPORTEURS ET CANAUX IONIQUES  
INVENTOR(S): BAUGHN, Mariah, R.;  
BURFORD, Neil;  
AU-YOUNG, Janice;  
LU, Dyung, Aina, M.;  
YANG, Junming;  
REDDY, Roopa;  
LAL, Preeti;  
HILLMAN, Jennifer, L.;  
AZIMZAI, Yalda;  
YUE, Henry;  
NGUYEN, Danniel, B.;  
YAO, Monique, G.;  
GANDHI, Ameena, R.;  
TANG, Y., Tom;  
KHAN, Farrah, A.

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W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU  
CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN  
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK  
MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM  
TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD  
SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY  
DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF  
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APPLICATION INFO.: WO 2000-US35095 A 20001222  
PRIORITY INFO.: US 1999-60/172,000 19991223  
US 2000-60/176,083 20000114  
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L6 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 1999254548 MEDLINE

DOCUMENT NUMBER: 99254548 PubMed ID: 10321245

TITLE: Inhalational anesthetics activate two-pore-domain background K<sup>+</sup> channels.

AUTHOR: Patel A J; Honore E; Lesage F; Fink M; Romey G; Lazdunski M

CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire-CNRS-UPR 411, Valbonne, France.

SOURCE: NATURE NEUROSCIENCE, (1999 May) 2 (5) 422-6.  
Journal code: 9809671. ISSN: 1097-6256.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199905

ENTRY DATE: Entered STN: 19990607  
Last Updated on STN: 19990607  
Entered Medline: 19990525

AB Volatile anesthetics produce safe, reversible unconsciousness, amnesia and analgesia via hyperpolarization of mammalian neurons. In molluscan pacemaker neurons, they activate an inhibitory synaptic K<sup>+</sup> current (IKAn), proposed to be important in general **anesthesia**. Here we show that TASK and **TREK-1**, two recently cloned mammalian two-P-domain K<sup>+</sup> channels similar to IKAn in biophysical properties, are activated by volatile general anesthetics. Chloroform, diethyl ether, halothane and isoflurane activated **TREK-1**, whereas only halothane and isoflurane activated TASK. Carboxy (C)-terminal regions were critical for anesthetic activation in both channels. Thus both **TREK-1** and TASK are possibly important target sites for these agents.

L17 ANSWER 16 OF 84 MEDLINE  
 ACCESSION NUMBER: 95355355 MEDLINE  
 DOCUMENT NUMBER: 95355355 PubMed ID: 7629068  
 TITLE: Amino terminus and the first four membrane-spanning segments of the Arabidopsis K<sup>+</sup> channel KAT1 confer inward-rectification property of plant-animal chimeric channels.  
 AUTHOR: Cao Y; Crawford N M; Schroeder J I  
 CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla 92093-0116, USA.  
 CONTRACT NUMBER: GM40672 (NIGMS)  
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jul 28) 270 (30) 17697-701.  
 Journal code: HIV; 2985121R. ISSN: 0021-9258.  
 PUB. COUNTRY: United States  
 Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 199509  
 ENTRY DATE: Entered STN: 19950921  
 Last Updated on STN: 19990129  
 Entered Medline: 19950905

AB The Arabidopsis hyperpolarization-activated (inward-rectifying) K<sup>+</sup> + **channel** KAT1 is structurally more similar to animal depolarization-activated (**outward**-rectifying) K<sup>+</sup> **channels** than to animal hyperpolarization-activated K<sup>+</sup> **channels**. To gain insight into the structural basis for the opposite voltage dependences of plant inward-rectifying and animal **outward**-rectifying K<sup>+</sup> **channels**, we constructed recombinant chimeric **channels** between the hyperpolarization-activated K<sup>+</sup> **channel** KAT1 and a Xenopus depolarization-activated K<sup>+</sup> **channel**. We report here that two of the chimeric constructs, which contain the first third of the KAT1 sequence, including the first four membrane-spanning segments (S1-S4) and the linker sequence between the fourth and fifth membrane-spanning segments, express functional channels that retain activation by hyperpolarization, but not depolarization. These two chimeric **channels** are no longer selective for K<sup>+</sup>. The chimeras are selective for cations over anions and are permeable to Ca<sup>2+</sup>. Therefore, unlike animal hyperpolarization-activated K<sup>+</sup> **channels**, in which the carboxyl terminus is important for inward rectification induced by Mg<sup>2+</sup> and polyamine block, the plant KAT1 channel has its major determinants for inward rectification in the amino-terminal region, which ends at the end of the S4-S5 linker.

**WEST****End of Result Set**

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11/15/96

L1: Entry 2 of 2

File: USPT

Jan 11, 2000

US-PAT-NO: 6013470

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

DATE-ISSUED: January 11, 2000

## INVENTOR-INFORMATION:

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Barhanin; Jacques	Nice			FR

US-CL-CURRENT: 435/69.1; 435/320.1, 435/325, 536/23.1

## CLAIMS:

We claim:

1. An isolated and purified nucleic acid molecule encoding a mammalian protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
2. An isolated and purified nucleic acid molecule encoding a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
3. The nucleic acid molecule of claim 2 encoding a human protein which exhibits weak inward rectification.
4. The nucleic acid molecule of claim 3 which is expressed in brain and heart tissue and in addition, in at least one of the following tissues: placenta, liver, skeletal, muscle, kidney and pancreas.
5. The human nucleic acid sequence of claim 2 which comprises the sequence represented by SEQ ID No. 1. *encodes SEQ ID NO. 5*
6. A self replication vector comprising the nucleic acid molecule of claim 2.
7. A cell transformed with the self replicating vector of claim 6, which cell expresses a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
8. A micro-injected cell comprising the RNA transcript synthesized from the nucleic acid molecule of claim 2, which cell expresses a human protein which

comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.

9. The transformed cell of claim 7, which cell is selected from the group consisting of prokaryotes and eukaryotes.

10. The transformed cell of claim 9 which is a bacterium.

11. The transformed cell of claim 10 which is a yeast, insect, plant or mammalian cell.

12. A method for the production of a human protein competent to transport potassium across a membrane which comprises 2 P domains and 4 transmembrane segments, comprising transferring the vector of claim 6 into a cellular host, culturing the cellular host under conditions allowing the production of said potassium channel, and purifying the human potassium channel.

13. The method of claim 12 wherein the cellular host is selected from the group consisting of prokaryotes and eukaryotes.

14. A pharmaceutical composition for the compensation of a deficiency in potassium channels at the level of one or more tissues, which comprises an isolated and purified nucleic acid molecule encoding a human protein comprising 2 P domains and 4 transmembrane segments which protein is competent to transport potassium across a membrane.

15. A pharmaceutical composition which comprises human cells transformed with the nucleic acid molecule of claim 2.

**WEST****End of Result Set**☐

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L4: Entry 1 of 1

File: USPT

Jan 11, 2000

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

US Patent No. (1):  
6013470Brief Summary Text (5):

The subunits of the voltage-dependent K<sup>sup.</sup> channels activated by depolarization (Kv families) and the calcium-dependent K<sup>sup.</sup> channels exhibit six hydrophobic transmembranal domains, one of which (S4) contains repeated positive charges which confer on these channels their sensitivity to voltage and, consequently, in their functional outward rectification (Logothetis, D. E. et al., 1992, Neuron, 8, 531-540; Bezanilla, F. and Stefani, E., 1994, Annu. Rev. Biophys. Biomol. Struct., 23, 819-846).